

## **RAW SEQUENCE LISTING**

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Application Serial Number: 10/014,363A  
Source: FW16  
Date Processed by STIC: 3/9/05

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IFW16

## RAW SEQUENCE LISTING

DATE: 03/09/2005

PATENT APPLICATION: US/10/014,363A

TIME: 11:47:16

Input Set : A:\Cd20805.app

Output Set: N:\CRF4\03092005\J014363A.raw

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3 <110> APPLICANT: BURG, JOSEF
4   ENGEL, ALFRED
5   FRANZE, REINHARD
6   HILGER, BERND
7   SCHURIG, HARTMUT E.
8   TISCHER, WILHELM
9   WOZNY, MANFRED
11 <120> TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
13 <130> FILE REFERENCE: CD 20805
15 <140> CURRENT APPLICATION NUMBER: 10/014,363A
16 <141> CURRENT FILING DATE: 2001-12-11
18 <150> PRIOR APPLICATION NUMBER: EP 00127891.0
19 <151> PRIOR FILING DATE: 2000-12-20
21 <160> NUMBER OF SEQ ID NOS: 17
23 <170> SOFTWARE: PatentIn Ver. 3.3
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 165
27 <212> TYPE: PRT
28 <213> ORGANISM: Homo sapiens
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31 Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu
32   1           5           10           15
34 Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His
35           20           25           30
37 Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe
38           35           40           45
40 Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp
41           50           55           60
43 Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu
44   65           70           75           80
46 Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp
47           85           90           95
49 Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
50           100          105          110
52 Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
53           115          120          125
55 Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val
56           130          135          140
58 Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala
59 145          150          155          160
61 Cys Arg Thr Gly Asp
62           165
65 <210> SEQ ID NO: 2

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66 <211> LENGTH: 166
67 <212> TYPE: PRT
68 <213> ORGANISM: Homo sapiens
70 <400> SEQUENCE: 2
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72   1           5           10           15
74 Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His
75           20           25           30
77 Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe
78           35           40           45
80 Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp
81           50           55           60
83 Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu
84   65           70           75           80
86 Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp
87           85           90           95
89 Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
90           100          105          110
92 Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
93           115          120          125
95 Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val
96           130          135          140
98 Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala
99 145          150          155          160
101 Cys Arg Thr Gly Asp Arg
102           165
106 <210> SEQ ID NO: 3
107 <211> LENGTH: 201
108 <212> TYPE: PRT
109 <213> ORGANISM: Artificial Sequence
111 <220> FEATURE:
112 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein
113     construct
115 <400> SEQUENCE: 3
116 Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
117   1           5           10           15
119 Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Ile
120           20           25           30
122 Glu Gly Arg Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu
123           35           40           45
125 Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys
126           50           55           60
128 Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys
129   65           70           75           80
131 Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val
132           85           90           95
134 Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly
135           100          105          110
137 Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu

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138      115      120      125
140 His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu
141      130      135      140
143 Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala
144 145      150      155      160
146 Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu
147      165      170      175
149 Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr
150      180      185      190
152 Gly Glu Ala Cys Arg Thr Gly Asp Arg
153      195      200
156 <210> SEQ ID NO: 4
157 <211> LENGTH: 196
158 <212> TYPE: PRT
159 <213> ORGANISM: Artificial Sequence
161 <220> FEATURE:
162 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein
163      construct
165 <400> SEQUENCE: 4
166 Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
167 1      5      10      15
169 Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Ala Pro
170      20      25      30
172 Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu
173      35      40      45
175 Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser
176      50      55      60
178 Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala
179 65      70      75      80
181 Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly
182      85      90      95
184 Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val
185      100      105      110
187 Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala
188      115      120      125
190 Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala
191      130      135      140
193 Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu
194 145      150      155      160
196 Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser
197      165      170      175
199 Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg
200      180      185      190
202 Thr Gly Asp Arg
203      195
206 <210> SEQ ID NO: 5
207 <211> LENGTH: 201
208 <212> TYPE: PRT
209 <213> ORGANISM: Artificial Sequence

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211 <220> FEATURE:
212 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein
213     construct
215 <400> SEQUENCE: 5
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217   1           5           10           15
219 Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Gly Ala
220           20           25           30
222 Ala His Tyr Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu
223           35           40           45
225 Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys
226           50           55           60
228 Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys
229   65           70           75           80
231 Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val
232           85           90           95
234 Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly
235           100          105          110
237 Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu
238           115          120          125
240 His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu
241           130          135          140
243 Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala
244   145          150          155          160
246 Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu
247           165          170          175
249 Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr
250           180          185          190
252 Gly Glu Ala Cys Arg Thr Gly Asp Arg
253           195          200
256 <210> SEQ ID NO: 6
257 <211> LENGTH: 629
258 <212> TYPE: DNA
259 <213> ORGANISM: Artificial Sequence
261 <220> FEATURE:
262 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic nucleotide
263     construct
265 <220> FEATURE:
266 <221> NAME/KEY: CDS
267 <222> LOCATION: (14)..(616)
269 <400> SEQUENCE: 6
270 ggaattcacc acc atg ggg gtg cac gaa tgt cct gcc tgg ctg tgg ctt      49
271           Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu
272           1           5           10
274 ctc ctg tcc ctg ctg tgc ctc cct ctg ggc ctc cca gtc ctg ggc gcc      97
275 Leu Leu Ser Leu Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala
276           15           20           25
278 ccc ccc cga atc gag ggc cgc gcc cca cca cgc ctc atc tgt gac agc     145
279 Pro Pro Arg Ile Glu Gly Arg Ala Pro Pro Arg Leu Ile Cys Asp Ser

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280      30      35      40
282 cga gtc ctg gag agg tac ctc ttg gag gcc aag gag gcc gag aat atc 193
283 Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile
284 45      50      55      60
286 acg acg ggc tgt gct gaa cac tgc agc ttg aat gag aat atc act gtc 241
287 Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val
288      65      70      75
290 cca gac acc aaa gtt aat ttc tat gcc tgg aag agg atg gag gtc ggg 289
291 Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly
292      80      85      90
294 cag cag gcc gta gaa gtc tgg cag ggc ctg gcc ctg ctg tcg gaa gct 337
295 Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala
296      95      100      105
298 gtc ctg cgg ggc cag gcc ctg ttg gtc aac tct tcc cag ccg tgg gag 385
299 Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu
300      110      115      120
302 ccc ctg cag ctg cat gtg gat aaa gcc gtc agt ggc ctt cgc agc ctc 433
303 Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu
304 125      130      135      140
306 acc act ctg ctt cgg gct ctg gga gcc cag aag gaa gcc atc tcc cct 481
307 Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro
308      145      150      155
310 cca gat gcg gcc tca gct gct cca ctc cga aca atc act gct gac act 529
311 Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr
312      160      165      170
314 ttc cgc aaa ctc ttc cga gtc tac tcc aat ttc ctc cgg gga aag ctg 577
315 Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu
316      175      180      185
318 aag ctg tac aca ggg gag gcc tgc agg aca ggg gac aga tgaccagggtc 626
319 Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg
320      190      195      200
322 gac 629
325 <210> SEQ ID NO: 7
326 <211> LENGTH: 614
327 <212> TYPE: DNA
328 <213> ORGANISM: Artificial Sequence
330 <220> FEATURE:
331 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
332 nucleotide construct
334 <220> FEATURE:
335 <221> NAME/KEY: CDS
336 <222> LOCATION: (14)..(601)
338 <400> SEQUENCE: 7
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340 Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu
341      1      5      10
343 ctc ctg tcc ctg ctg tcg ctc cct ctg ggc ctc cca gtc ctg ggc gcc 97
344 Leu Leu Ser Leu Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala
345      15      20      25

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**VERIFICATION SUMMARY**

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